SEQUENCE LISTING

<110> Merck & Co., Inc.

LaMonica, Nicola

Facciabene, Andrea

Aurisicchio, Luigi

<120> CARCINOEMBRYONIC ANTIGEN FUSIONS AND

USES THEREOF

<130> ITR0073YP

<150> PCT/EP2005/001114
<151> 2005-02-03

<150> 60/635,791
<151> 2004-12-14

<150> 60/543,649
<151> 2004-02-11

<160> 54

<170> FastSEQ for Windows Version 4.0

<210> 1
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<220>
<223> PCR Primer

<400> 1
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<211> 35
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<213> {PArtificial Sequence


<220>
<223> PCR Primer


<400> 2
tatgcggccg cctagttttc catactgatt gccgc                                35


<210> 3
<211> 35
<212> DNA
<213> Artificial Sequence


<220>
<223> PCR Primer


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gctctagagc cccccagagc atcaccgagc tgtgc                                35


<210> 4
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<212> DNA
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<220>
<223> PCR Primer


<400> 4
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<210> 5
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<212> DNA
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<213> Artificial Sequence

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<223> PCR Primer

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<210> 6
<211> 35
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<220>
<223> PCR Primer

<400> 6
tatgcggccg ctcataattc atcccgaatt ctgtt   35

<210> 7
<211> 2766
<212> DNA
<213> Artificial Sequence

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<223> CEA-LTA fusion

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acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata 300
atataccccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaacccgt ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540

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aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600

actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660

gtgagtgcca ggcgcagtga ttcagtcatc ctgaatgtcc tctatggccc ggatgccccc 720

accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctcctgccac 780

gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840

acccaagagc tctttatccc caacatcact gtgaataata gtggatccta cgtgccaa 900

gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960

gagccaccca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020

gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg ggtaaataat 1080

cagagcctcc cggtcagtcc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140

ctcagtgtca caaggaatga tgtaggaccc tatgagtgtg aatccagaa cgaattaagt 1200

gttgaccaca gcgacccagt catcctgaat gtcctctatg cccagacga ccccaccatt 1260

tccccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg ccatgcagcc 1320

tctaacccac ctgcacagta ttcttggctg attgatggga acatccagca acacacacaa 1380

gagctcttta tctccaacat cactgagaag aacagcggac tctatacctg ccaggccaat 1440

aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgcggagctg 1500

cccaagccct ccatctccag caacaactcc aaacccgtgg aggacaagga tgctgtggcc 1560

ttcacctgtg aacctgaggc tcagaacaca acctacctgt ggtgggtaaa tggtcagagc 1620

ctcccagtca gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680

gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gagtgcaaac 1740

cgcagtgacc cagtcaccct ggatgtcctc tatgggccgg acacccccat catttccccc 1800

ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggcctctaac 1860

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gctactggcc gcaataattc catagtcaag agcatcacag tctctgcatc tggaactcta 2040

gttaatggcg acaaattata ccgtgctgac tctagacccc cagatgaaat aaaacgttcc 2100

ggaggtctta tgcccagagg gcataatgag tacttcgata gaggaactca aatgaatatt 2160

aatctttatg atcacgcgag aggaacacaa accggctttg tcagatatga tgacggatat 2220

gtttccactt ctcttagttt gagaagtgct cacttagcag acagtctat attatcagga 2280

tattccactt actatatata tgttatagcg acagcaccaa atatgtttaa tgttaatgat 2340

gtattaggcg tatacagccc tcacccatat gaacaggagg tttctgcgtt aggtggaata 2400

ccatattctc agatatatgg atggtatcgt gttaattttg gtgtaattga tgaacgatta 2460

catcgtaaca gggaatatag agaccggtat tacagaaatc tgaatatagc tccggcagag 2520

gatggttaca gattagcagg tttcccaccg gatcaccaag cttggagaga agaaccctgg 2580

attcatcatg caccacaagg ttgtggaaat tcatcaagaa caattacaga tgatacttgt 2640

aatgaggaga cccagaatct gagcacaata tatctcagga aatatcaatc aaaagttaag 2700

aggcagatat tttcagacta tcagtcagag gttgacatat ataacagaat tcgggatgaa 2760
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ttatga   2766

<210> 8

<211> 921

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 8

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
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Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20   25   30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
        35   40   45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
    50   55   60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65   70   75   80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
                85   90   95

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
            100   105   110

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
            115   120   125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
    130   135   140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145   150   155   160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
                165   170   175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180   185   190

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
            195   200   205

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Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
    210                 215                 220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                 230                 235                 240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
                245                 250                 255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
                260                 265                 270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
            275                 280                 285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
    290                 295                 300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305                 310                 315                 320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325                 330                 335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
                340                 345                 350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
            355                 360                 365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
    370                 375                 380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385                 390                 395                 400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                405                 410                 415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
                420                 425                 430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
            435                 440                 445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
    450                 455                 460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                 470                 475                 480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
            485                 490                 495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
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            500                    505                    510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
        515                    520                    525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
        530                    535                    540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545                    550                    555                    560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
                565                    570                    575
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
                580                    585                    590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
            595                    600                    605
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
        610                    615                    620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625                    630                    635                    640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                645                    650                    655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
                660                    665                    670
Thr Val Ser Ala Ser Gly Thr Leu Val Asn Gly Asp Lys Leu Tyr Arg
                675                    680                    685
Ala Asp Ser Arg Pro Pro Asp Glu Ile Lys Arg Ser Gly Gly Leu Met
        690                    695                    700
Pro Arg Gly His Asn Glu Tyr Phe Asp Arg Gly Thr Gln Met Asn Ile
705                    710                    715                    720
Asn Leu Tyr Asp His Ala Arg Gly Thr Gln Thr Gly Phe Val Arg Tyr
                725                    730                    735
Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser Leu Arg Ser Ala His Leu
                740                    745                    750
Ala Gly Gln Ser Ile Leu Ser Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val
        755                    760                    765
Ile Ala Thr Ala Pro Asn Met Phe Asn Val Asn Asp Val Leu Gly Val
        770                    775                    780
Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu Gly Gly Ile
785                    790                    795                    800
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Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe Gly Val Ile
                 805                 810                 815
Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg
                 820                 825                 830
Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu Ala Gly Phe
                 835                 840                 845
Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile His His Ala
             850                 855                 860
Pro Gln Gly Cys Gly Asn Ser Ser Arg Thr Ile Thr Asp Asp Thr Cys
865                 870                 875                 880
Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg Lys Tyr Gln
                 885                 890                 895
Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser Glu Val Asp
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Ile Tyr Asn Arg Ile Arg Asp Glu Leu
                 915                 920
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<210> 9
<211> 2355
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA-LTB fusion

<400> 9
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acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata 300
atataccccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaacccgt ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
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actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660
gtgagtgcca ggcgcagtga ttcagtcatc ctgaatgtcc tctatggccc ggatgccccc 720
accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctcctgccac 780
gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgccaa 900
gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
gagccaccca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg ggtaaataat 1080
cagagcctcc cggtcagtcc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140
ctcagtgtca caaggaatga tgtaggaccc tatgagtgtg gaatccagaa cgaattaagt 1200
gttgaccaca gcgacccagt catcctgaat gtcctctatg cccagacga ccccaccatt 1260
tcccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg ccatgcagcc 1320
tctaacccac ctgcacagta ttcttggctg attgatggga acatccagca acacacacaa 1380
gagctcttta tctccaacat cactgagaag aacagcggac tctatacctg ccaggccaat 1440
aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgcggagctg 1500
cccaagccct ccatctccag caacaactcc aaacccgtgg aggacaagga tgctgtggcc 1560
ttcacctgtg aacctgaggc tcagaacaca acctacctgt ggtgggtaaa tggtcagagc 1620
ctcccagtca gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680
gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gagtgcaaac 1740
cgcagtgacc cagtcaccct ggatgtcctc tatgggccgg acaccccat catttccccc 1800
ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggcctctaac 1860
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gctactggcc gcaataattc catagtcaag agcatcacag tctctgcatc tggaactcta 2040
gatgctcccc agtctattac agaactatgt tcggaatatc gcaacacaca aatatatacg 2100
ataaatgaca agatactatc atatacggaa tcgatggcag gtaaaagaga aatggttatc 2160
attacattta agagcggcgc aacatttcag gtcgaagtcc cgggcagtca acatatagac 2220
tcccaaaaaa aagccattga aaggatgaag gacacattaa gaatcacata tctgaccgag 2280
accaaaattg ataaattatg tgtatggaat aataaaaccc ccaattcaat tgcggcaatc 2340
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<210> 10
<211> 784
<212> PRT
<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 10

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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
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Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20                  25                  30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
        35                  40                  45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
    50                  55                  60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65                  70                  75                  80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
                85                  90                  95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
            100                 105                 110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
            115                 120                 125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
    130                 135                 140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145                 150                 155                 160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
                165                 170                 175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180                 185                 190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
            195                 200                 205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
        210                 215                 220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                 230                 235                 240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
                245                 250                 255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
            260                 265                 270
```

```
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
        275             280             285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
        290             295             300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305             310             315             320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325             330             335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
            340             345             350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
        355             360             365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
    370             375             380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385             390             395             400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
            405             410             415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
            420             425             430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
        435             440             445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
    450             455             460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465             470             475             480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
            485             490             495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
            500             505             510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
        515             520             525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
    530             535             540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545             550             555             560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
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                    565                    570                    575
   Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
                580                    585                    590
   Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
                    595                    600                    605
   Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
                610                    615                    620
   Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
   625                    630                    635                    640
   Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                    645                    650                    655
   Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
                660                    665                    670
   Thr Val Ser Ala Ser Gly Thr Leu Asp Ala Pro Gln Ser Ile Thr Glu
                    675                    680                    685
   Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys
                690                    695                    700
   Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile
   705                    710                    715                    720
   Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser
                    725                    730                    735
   Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
                    740                    745                    750
   Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val
                755                    760                    765
   Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
                770                    775                    780
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<210> 11
<211> 2355
<212> DNA
<213> Artificial Sequence

<220>
<223> CEAopt-LTB fusion

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<400> 11

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accccttca acgtggccga gggcaaggag gtgctgctgc tggtgcacaa cctgccccag 180

cacctgttcg gctacagctg gtacaagggc gagcgcgtgg acggcaaccg ccagatcatc 240

ggctacgtga tcggcaccca gcaggccacc cccggccccg cctacagcgg ccgcgagatc 300

atctacccca cgccagcct gctgatccag aacatcatcc agaacgacac cggcttctac 360

accctgcacg tgatcaagag cgacctggtg aacgaggagg ccaccggcca gttccgcgtg 420

taccccgagc tgcccaagcc cagcatcagc agcaacaaca gcaagcccgt ggaggacaag 480

gacgccgtgg ccttcacctg cgagcccgag acccaggacg ccacctacct gtggtgggtg 540

aacaaccaga gcctgcccgt gagcccccgc ctgcagctga gcaacggcaa ccgcaccctg 600

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gcccacaaca gcgacaccgg cctgaaccgc accaccgtga ccaccatcac cgtgtacgcc 960

gagcccccca gcccttcat caccagcaac aacagcaacc ccgtggagga cgaggacgcc 1020

gtggccctga cctgcgagcc cgagatccag aacaccacct acctgtggtg ggtgaacaac 1080

cagagcctgc ccgtgagccc ccgcctgcag ctgagcaacg acaaccgcac cctgaccctg 1140

ctgagcgtga cccgcaacga cgtgggcccc tacgagtgcg gcatccagaa cgagctgagc 1200

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agcaaccccc cgcccagta cagctggctg atcgacggca acatccagca gcacacccag 1380

gagctgttca tcagcaacat caccgagaag aacagcggcc tgtacacctg ccaggccaac 1440

aacagcgcca gcggccacag ccgcaccacc gtgaagacca tcaccgtgag cgccgagctg 1500

cccaagccca gcatcagcag caacaacagc aagcccgtgg aggacaagga cgccgtggcc 1560

ttcacctgcg agcccgaggc ccagaacacc acctacctgt ggtgggtgaa cggccagagc 1620

ctgcccgtga gccccgcct gcagctgagc aacggcaacc gcaccctgac cctgttcaac 1680

gtgacccgca cgacgcccg cgcctacgtg tgcggcatcc agaacagcgt gagcgccaac 1740

cgcagcgacc ccgtgaccct ggacgtgctg tacggccccg acacccccat catcagcccc 1800

cccgacagca gctacctgag cggcgccaac ctgaacctga gctgccacag cgccagcaac 1860

cccagcccc agtacagctg gcgcatcaac ggcatccccc agcagcacac ccaggtgctg 1920

ttcatcgcca agatcacccc caacaacaac ggcacctacg cctgcttcgt gagcaacctg 1980

gccaccggcc gcaacaacag catcgtgaag agcatcaccg tgagcgccag cggcacctct 2040

agagctcccc agactattac agaactatgt tcggaatatc gcaacacaca aatatatacg 2100

ataaatgaca agatactatc atatacggaa tcgatggcag gcaaaagaga aatggttatc 2160

```
attacattta agagcggcga aacatttcag gtcgaagtcc cgggcagtca acatatagac 2220
tcccagaaaa aagccattga aaggatgaag gacacattaa gaatcacata tctgaccgag 2280
accaaaattg ataaattatg tgtatggaat aataaaaccc ccaattcaat tgcggcaatc 2340
agtatggaaa actag                                                  2355
```

<210> 12
<211> 2358
<212> DNA
<213> Artificial Sequence

<220>
<223> CEAopt-LTBopt fusion

<400> 12
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atggagagcc ccagcgcccc cccccaccgc tggtgcatcc cctggcagcg cctgctgctg 60
accgccagcc tgctgacctt ctggaacccc cccaccaccg ccaagctgac catcgagagc 120
accccctta acgtggccga gggcaaggag gtgctgctgc tggtgcacaa cctgccccag 180
cacctgttcg gctacagctg gtacaagggc gagcgcgtgg acggcaaccg ccagatcatc 240
ggctacgtga tcggcaccca gcaggccacc cccggccccg cctacagcgg ccgcgagatc 300
atctacccca cgccagcct gctgatccag aacatcatcc agaacgacac cggcttctac 360
accctgcacg tgatcaagag cgacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccccgagc tgcccaagcc cagcatcagc agcaacaaca gcaagcccgt ggaggacaag 480
gacgccgtgg ccttcacctg cgagcccgag acccaggacg ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccgt gagcccccgc ctgcagctga gcaacggcaa ccgcaccctg 600
accctgttca acgtgacccg caacgacacc gccagctaca agtgcgagac ccagaacccc 660
gtgagcgccc ccgcagcga gcgtgatc ctgaacgtgc tgtacggccc cgacgccccc 720
accatcagcc ccctgaacac cagctaccgc agcggcgaga acctgaacct gagctgccac 780
gccgccagca accccccgc ccagtacagc tggttcgtga cggcaccctt ccagcagagc 840
acccaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta cacctgccag 900
gcccacaaca gcgacaccgg cctgaaccgc accaccgtga ccaccatcac cgtgtacgcc 960
gagcccccca gcccttcat caccagcaac aacagcaacc ccgtggagga cgaggacgcc 1020
gtggccctga cctgcgagcc cgagatccag aacaccacct acctgtggtg ggtgaacaac 1080
cagagcctgc ccgtgagccc ccgcctgcag ctgagcaacg acaaccgcac cctgacccctg 1140
ctgagcgtga cccgcaacga cgtgggcccc tacgagtgcg gcatccagaa cgagctgagc 1200
gtggaccaca gcgaccccgt gatcctgaac gtgctgtacg ccccgacga ccccaccatc 1260
agccccagct acacctacta ccgcccctggc gtgaacctga gcctgagctg ccacgccgcc 1320
agcaaccccc ccgcccagta cagctggctg atcgacggca acatccagca gcacacccag 1380
```

```
gagctgttca tcagcaacat caccgagaag aacagcggcc tgtacacctg ccaggccaac 1440

aacagcgcca gcggccacag ccgcaccacc gtgaagacca tcaccgtgag cgccgagctg 1500

cccaagccca gcatcagcag caacaacagc aagcccgtgg aggacaagga cgccgtggcc 1560

ttcacctgcg agcccgaggc ccagaacacc acctacctgt ggtgggtgaa cggccagagc 1620

ctgcccgtga gcccccgcct gcagctgagc aacggcaacc gcaccctgac cctgttcaac 1680

gtgacccgca cgacgcccg cgcctacgtg tgcggcatcc agaacagcgt gagcgccaac 1740

cgcagcgacc ccgtgaccct ggacgtgctg tacggccccg acacccccat catcagcccc 1800

cccgacagca gctacctgag cggcgccaac ctgaacctga gctgccacag cgccagcaac 1860

cccagccccc agtacagctg cgcatcaac ggcatccccc agcagcacac ccaggtgctg 1920

ttcatcgcca agatcacccc caacaacaac ggcacctacg cctgcttcgt gagcaacctg 1980

gccaccggcc gcaacaacag catcgtgaag agcatcaccg tgagcgccag cggcacctct 2040

agagcccccc agagcatcac cgagctgtgc agcgagtacc ggaacaccca gatctacacc 2100

atcaacgaca agatcctgag ctacaccgag agcatggccg gcaagaggga gatggtgatc 2160

atcaccttca gagcggcgc caccttccag gtggaggtgc ccggcagcca gcacatcgac 2220

agccagaaga aggccatcga gcggatgaag gacaccctgc ggatcaccta cctcaccgag 2280

accaagatcg acaagctgtg cgtgtggaac aacaagaccc ccaacagcat cgccgccatc 2340

agcatggaga attgataa                                                  2358
```

```
<210> 13
<211> 784
<212> PRT
<213> Artificial Sequence

<220>
<223> CEAopt-LTBopt fusion

<400> 13
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1               5                   10                  15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20                  25                  30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
        35                  40                  45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
    50                  55                  60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65                  70                  75                  80
```

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
                    85   90   95

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
                    100   105   110

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
                115   120   125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
            130   135   140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145   150   155   160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
                165   170   175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
                180   185   190

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
                195   200   205

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
        210   215   220

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225   230   235   240

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
                245   250   255

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
                260   265   270

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
            275   280   285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
        290   295   300

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305   310   315   320

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325   330   335

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
            340   345   350

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
            355   360   365

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr

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```
          370                 375                 380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385                 390                 395                 400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                405                 410                 415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
                420                 425                 430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
                435                 440                 445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
        450                 455                 460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                 470                 475                 480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
                485                 490                 495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
                500                 505                 510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
                515                 520                 525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
        530                 535                 540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545                 550                 555                 560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
                565                 570                 575
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
                580                 585                 590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
                595                 600                 605
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
        610                 615                 620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625                 630                 635                 640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                645                 650                 655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
                660                 665                 670
```

```
Thr Val Ser Ala Ser Gly Thr Ser Arg Ala Pro Gln Ser Ile Thr Glu
        675             680             685
Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys
        690             695             700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile
705             710             715             720
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser
            725             730             735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
            740             745             750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val
        755             760             765
Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
        770             775             780
```

```
<210> 14
<211> 2358
<212> DNA
<213> Artificial Sequence

<220>
<223> rhCEAopt-LTBopt fusion

<400> 14
atgggcagcc ccagcgcccc cctgcaccgc tggtgcatcc cctggcagac cctgctgctg 60
accgccagcc tgctgacctt ctggaacccc cccaccaccg cccagctgac catcgagagc 120
cgccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
aacctgttcg gctacatctg tacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
agctgcgtga tccgcaccca gcagatcacc cccggccccg cccacagcgg ccgcgagacc 300
atcgacttca cgccagcct gctgatccac aacgtgaccc agagcgacac cggcagctac 360
accatccagg tgatcaagga ggacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccccgagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccgt ggaggacaag 480
gacgccgtgg ccctgacctg cgagcccgag acccaggaca ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccgt gagcccccgc ctggagctga gcagcgacaa ccgcaccctg 600
accgtgttca acatcccccg caacgacacc accagctaca gtgcgagac ccagaacccc 660
gtgagcgtgc gccgcagcga ccccgtgacc ctgaacgtgc tgtacggccc cgacgccccc 720
```

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```
accatcagcc ccctgaacac cccctaccgc gccggcgaga acctgaacct gacctgccac 780

gccgccagca accccaccgc ccagtacttc tggttcgtga acggcacctt ccagcagagc 840

acccaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta catgtgccag 900

gcccacaaca gcgccaccgg cctgaaccgc accaccgtga ccgccatcac cgtgtacgcc 960

gagctgccca gccctacat caccagcaac aacagcaacc ccatcgagga caaggacgcc 1020

gtgaccctga cctgcgagcc cgagacccag gacaccacct acctgtggtg ggtgaacaac 1080

cagagcctga gcgtgagcag ccgcctggag ctgagcaacg acaaccgcac cctgaccgtg 1140

ttcaacatcc cccgcaacga caccaccttc tacgagtgcg agacccagaa ccccgtgagc 1200

gtgcgccgca gcgaccccgt gaccctgaac gtgctgtacg gccccgacgc ccccaccatc 1260

agccccctga acacccccta ccgcgccggc gagaacctga acctgagctg ccacgccgcc 1320

agcaaccccg ccgcccagta cagctggttc gtgaacggca ccttccagca gagcacccag 1380

gagctgttca tccccaacat caccgtgaac aacagcggca gctacatgtg ccaggcccac 1440

aacagcgcca ccggcctgaa ccgcaccacc gtgaccgcca tcaccgtgta cgtggagctg 1500

cccaagccct acatcagcag caacaacagc aaccccatcg aggacaagga cgccgtgacc 1560

ctgacctgcg agcccgtggc cgagaacacc acctacctgt ggtgggtgaa caaccagagc 1620

ctgagcgtga gcccccgcct gcagctgagc aacggcaacc gcatcctgac cctgctgagc 1680

gtgacccgca cgacaccgg ccccctacgag tgcggcatcc agaacagcga gagcgccaag 1740

cgcagcgacc ccgtgaccct gaacgtgacc tacggccccg acccccccat catcagcccc 1800

cccgacctga gctaccgcag cggcgccaac ctgaacctga gctgccacag cgacagcaac 1860

cccagccccc agtacagctg gctgatcaac ggcacccctgc gccagcacac ccaggtgctg 1920

ttcatcagca agatcaccag caacaacagc ggcgcctacg cctgcttcgt gagcaacctg 1980

gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040

agagcccccc agagcatcac cgagctgtgc agcgagtacc ggaacaccca gatctacacc 2100

atcaacgaca agatcctgag ctacaccgag agcatggccg gcaagaggga gatggtgatc 2160

atcaccttca gagcggcgc caccttccag gtggaggtgc ccggcagcca gcacatcgac 2220

agccagaaga aggccatcga gcggatgaag gacaccctgc ggatcaccta cctcaccgag 2280

accaagatcg acaagctgtg cgtgtggaac aacaagaccc ccaacagcat cgccgccatc 2340

agcatggaga attgataa                                                 2358
```

<210> 15
<211> 784
<212> PRT
<213> Artificial Sequence

<220>
<223> rhCEAopt-LTBopt fusion

<400> 15

Met	Gly	Ser	Pro	Ser	Ala	Pro	Leu	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
1				5					10					15	

| Thr | Leu | Leu | Leu | Thr | Ala | Ser | Leu | Leu | Thr | Phe | Trp | Asn | Pro | Pro | Thr |
| | | | 20 | | | | | 25 | | | | 30 | | | |

| Thr | Ala | Gln | Leu | Thr | Ile | Glu | Ser | Arg | Pro | Phe | Asn | Val | Ala | Glu | Gly |
| | | 35 | | | | 40 | | | | | 45 | | | | |

| Lys | Glu | Val | Leu | Leu | Leu | Ala | His | Asn | Val | Ser | Gln | Asn | Leu | Phe | Gly |
| | 50 | | | | 55 | | | | | 60 | | | | | |

| Tyr | Ile | Trp | Tyr | Lys | Gly | Glu | Arg | Val | Asp | Ala | Ser | Arg | Arg | Ile | Gly |
| 65 | | | | 70 | | | | 75 | | | | | 80 | | |

| Ser | Cys | Val | Ile | Arg | Thr | Gln | Gln | Ile | Thr | Pro | Gly | Pro | Ala | His | Ser |
| | | | 85 | | | | 90 | | | | | 95 | | | |

| Gly | Arg | Glu | Thr | Ile | Asp | Phe | Asn | Ala | Ser | Leu | Leu | Ile | His | Asn | Val |
| | | 100 | | | | 105 | | | | | 110 | | | | |

| Thr | Gln | Ser | Asp | Thr | Gly | Ser | Tyr | Thr | Ile | Gln | Val | Ile | Lys | Glu | Asp |
| | | 115 | | | | 120 | | | | | 125 | | | | |

| Leu | Val | Asn | Glu | Glu | Ala | Thr | Gly | Gln | Phe | Arg | Val | Tyr | Pro | Glu | Leu |
| | 130 | | | | 135 | | | | | 140 | | | | | |

| Pro | Lys | Pro | Tyr | Ile | Ser | Ser | Asn | Asn | Ser | Asn | Pro | Val | Glu | Asp | Lys |
| 145 | | | | 150 | | | | 155 | | | | | 160 | | |

| Asp | Ala | Val | Ala | Leu | Thr | Cys | Glu | Pro | Glu | Thr | Gln | Asp | Thr | Thr | Tyr |
| | | | 165 | | | | 170 | | | | 175 | | | | |

| Leu | Trp | Trp | Val | Asn | Asn | Gln | Ser | Leu | Pro | Val | Ser | Pro | Arg | Leu | Glu |
| | | | 180 | | | | 185 | | | | 190 | | | | |

| Leu | Ser | Ser | Asp | Asn | Arg | Thr | Leu | Thr | Val | Phe | Asn | Ile | Pro | Arg | Asn |
| | | 195 | | | | 200 | | | | | 205 | | | | |

| Asp | Thr | Thr | Ser | Tyr | Lys | Cys | Glu | Thr | Gln | Asn | Pro | Val | Ser | Val | Arg |
| | 210 | | | | 215 | | | | 220 | | | | | | |

| Arg | Ser | Asp | Pro | Val | Thr | Leu | Asn | Val | Leu | Tyr | Gly | Pro | Asp | Ala | Pro |
| 225 | | | | 230 | | | | 235 | | | | | 240 | | |

| Thr | Ile | Ser | Pro | Leu | Asn | Thr | Pro | Tyr | Arg | Ala | Gly | Glu | Asn | Leu | Asn |
| | | | 245 | | | | 250 | | | | 255 | | | | |

| Leu | Thr | Cys | His | Ala | Ala | Ser | Asn | Pro | Thr | Ala | Gln | Tyr | Phe | Trp | Phe |
| | | 260 | | | | 265 | | | | | 270 | | | | |

| Val | Asn | Gly | Thr | Phe | Gln | Gln | Ser | Thr | Gln | Glu | Leu | Phe | Ile | Pro | Asn |
| | 275 | | | | 280 | | | | | 285 | | | | | |

```
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
    290             295             300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
305             310             315             320
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
            325             330             335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
            340             345             350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
        355             360             365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
    370             375             380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
385             390             395             400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
            405             410             415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
            420             425             430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
    435             440             445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
    450             455             460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
465             470             475             480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
            485             490             495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
            500             505             510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
            515             520             525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
    530             535             540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
545             550             555             560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
            565             570             575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
```

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```
              580                      585                      590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
              595                      600                  605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
         610                 615                 620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
625                      630                 635                  640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
                  645                 650                 655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
              660                 665                 670
Ser Val Ser Ser Gly Asp Ser Ser Arg Ala Pro Gln Ser Ile Thr Glu
         675                 680                 685
Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys
         690                 695                 700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile
705                 710                 715                      720
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser
                  725                 730                 735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
              740                 745                 750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val
              755                 760                 765
Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
         770                 775                 780
```

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<210> 16
<211> 2118
<212> DNA
<213> Macaca mulatta

<400> 16
atggggtctc cctcagcccc tcttcacaga tggtgcatcc cctggcagac gctcctgctc  60
acagcctcac ttctaacctt ctggaacccg cccaccactg cccagctcac tattgaatcc  120
aggccgttca atgttgcaga ggggaaggag gttcttctac ttgcccacaa tgtgtcccag  180
aatctttttg gctacatttg gtacaaggga gaaagagtgg atgccagccg tcgaattgga  240
```

```
tcatgtgtaa taagaactca acaaattacc ccagggcccg cacacagcgg tcgagagaca 300

atagacttca atgcatccct gctgatccac aatgtcaccc agagtgacac aggatcctac 360

accatacaag tcataaagga agatcttgtg aatgaagaag caactggcca gttccgggta 420

tacccggagc tgcccaagcc ctacatctcc agcaacaact ccaaccccgt ggaggacaag 480

gatgctgtgg ccttaacctg tgaacctgag actcaggaca caacctacct gtggtgggta 540

aacaatcaga gcctcccggt cagtcccagg ctggagctgt ccagtgacaa caggaccctc 600

actgtattca atattccaag aaatgacaca acatcctaca aatgtgaaac ccagaaccca 660

gtgagtgtca gacgcagcga cccagtcacc ctgaacgtcc tctatggccc ggatgcgccc 720

accatttccc ctctaaacac accttacaga gcaggggaaa atctgaacct cacctgccac 780

gcagcctcta acccaactgc acagtacttt tggtttgtca atgggacgtt ccagcaatcc 840

acacaagagc tctttatacc caacatcacc gtgaataata gcggatccta tatgtgccaa 900

gcccataact cagccactgg cctcaatagg accacagtca cggcgatcac agtctacgcg 960

gagctgccca gccctacat caccagcaac aactccaacc ccatagagga caaggatgct 1020

gtgaccttaa cctgtgaacc tgagactcag gacacaacct acctgtggtg ggtaaacaat 1080

cagagcctct cggtcagttc caggctggag ctgtccaatg acaacaggac cctcactgta 1140

ttcaatattc caagaaacga cacaacgttc tacgaatgtg agacccagaa cccagtgagt 1200

gtcagacgca gcgacccagt caccctgaat gtcctctatg gcccggatgc gcccaccatt 1260

tcccctctaa acacaccta cagagcaggg gaaaatctga acctctcctg ccacgcagcc 1320

tctaacccag ctgcacagta ctcttggttt gtcaatggga cgttccagca atccacacaa 1380

gagctcttta tacccaacat caccgtgaat aatagcggat cctatatgtg ccaagcccat 1440

aactcagcca ctggcctcaa taggaccaca gtcacggcga tcacagtcta tgtggagctg 1500

cccaagccct acatctccag caacaactcc aaccccatag aggacaagga tgctgtgacc 1560

ttaacctgtg aacctgtggc tgagaacaca acctacctgt ggtgggtaaa caatcagagc 1620

ctctcggtca gtcccaggct gcagctctcc aatggcaaca ggatcctcac tctactcagt 1680

gtcacacgga atgacacagg accctatgaa tgtggaatcc agaactcaga gagtgcaaaa 1740

cgcagtgacc cagtcaccct gaatgtcacc tatggcccag acaccccat catatccccc 1800

ccagacttgt cttaccgttc gggagcaaac ctcaacctct cctgccactc ggactctaac 1860

ccatccccgc agtattcttg cttatcaat gggacactgc ggcaacacac acaagttctc 1920

tttatctcca aaatcacatc aaacaatagc ggggcctatg cctgttttgt ctctaacttg 1980

gctaccggtc gcaataactc catagtcaag aacatctcag tctcctctgg cgattcagca 2040

cctggaagtt ctggtctctc agctagggct actgtcggca tcataattgg aatgctggtt 2100

ggggttgctc tgatgtag                                             2118
```

<210> 17

<211> 2118

<212> DNA

<213> Macaca mulatta

<400> 17

```
atggggtctc cctcagcccc tcttcacaga tggtgcatcc cctggcagac gctcctgctc 60

acagcctcac ttctaacctt ctggaacccg cccaccactg cccagctcac tattgaatcc 120

aggccgttca atgttgcaga ggggaaggag gttcttctac ttgcccacaa tgtgtcccag 180

aatctttttg gctacatttg gtacaaggga gaaagagtgg atgccagccg tcgaattgga 240

tcatgtgtaa taagaactca acaaattacc ccagggcccg cacacagcgg tcgagagaca 300

atagacttca atgcatccct gctgatccac aatgtcaccc agagtgacac aggatcctac 360

accatacaag tcataaagga agatcttgtg aatgaagaag caactggcca gttccgggta 420

tacccggagc tgcccaagcc ctacatctcc agcaacaact ccaaccccgt ggaggacaag 480

gatgctgtgg ccttaacctg tgaacctgag actcaggaca caacctacct gtggtgggta 540

aacaatcaga gcctcccggt cagtcccagg ctggagctgt ccagtgacaa caggaccctc 600

actgtattca atattccaag aaatgacaca acatcctaca atgtgaaac ccagaaccca 660

gtgagtgtca gacgcagcga cccagtcacc ctgaacgtcc tctatggccc ggatgcgccc 720

accatttccc ctctaaacac accttacaga gcaggggaaa atctgaacct cacctgccac 780

gcagcctcta acccaactgc acagtacttt tggtttgtca atgggacgtt ccagcaatcc 840

acacaagagc tctttatacc caacatcacc gtgaataata gcggatccta tatgtgccaa 900

gcccataact cagccactgg cctcaatagg accacagtca cggcgatcac agtctacgcg 960

gagctgccca gccctacat caccagcaac aactccaacc ccatagagga caaggatgct 1020

gtgaccttaa cctgtgaacc tgagactcag gacacaacct acctgtggtg ggtaaacaat 1080

cagagcctct cggtcagttc caggctggag ctgtccaatg acaacaggac cctcactgta 1140

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gtcagacgca gcgacccagt caccctgaat gtcctctatg cccggatgc gcccaccatt 1260

tcccctctaa acacacctta cagagcaggg gaaaatctga acctctcctg ccacgcagcc 1320

tctaacccag ctgcacagta cttttggttt gtcaatggga cgttccagca atccacacaa 1380

gagctcttta tacccaacat caccgtgaat aatagcggat cctatatgtg ccaagcccat 1440

aactcagcca ctggcctcaa taggaccaca gtcacggcga tcacagtcta tgtggagctg 1500

cccaagccct acatctccag caacaactcc aaccccatag aggacaagga tgctgtgacc 1560

ttaacctgtg aacctgtggc tgagaacaca acctacctgt ggtgggtaaa caatcagagc 1620

ctctcggtca gtcccaggct gcagctctcc aatggcaaca ggatcctcac tctactcagt 1680

gtcacacgga atgacacagg accctatgaa tgtggaatcc agaactcaga gagtgcaaaa 1740

cgcagtgacc cagtcaccct gaatgtcacc tatggcccag acacccccat catatccccc 1800

ccagacttgt cttaccgttc gggagcaaac ctcaacctct cctgccactc ggactctaac 1860

ccatccccgc agtattcttg cttatcaat gggacactgc ggcaacacac acaagttctc 1920

tttatctcca aaatcacatc aaacaataac ggggcctatg cctgtttgt ctctaacttg 1980

gctaccggtc gcaataactc catagtcaag aacatctcag tctcctctgg cgattcagca 2040

cctggaagtt ctggtctctc agctagggct actgtcggca tcataattgg aatgctggtt 2100
```

```
ggggttgctc tgatgtag                                                    2118
```

<210> 18
<211> 705
<212> PRT
<213> Macaca mulatta

<400> 18

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Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
1               5                   10                  15
Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20                  25                  30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
        35                  40                  45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
    50                  55                  60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65                  70                  75                  80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
                85                  90                  95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
            100                 105                 110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
            115                 120                 125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
    130                 135                 140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                 150                 155                 160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
                165                 170                 175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
            180                 185                 190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
            195                 200                 205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
    210                 215                 220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
```

```
      225                         230                         235                         240
Thr  Ile  Ser  Pro  Leu  Asn  Thr  Pro  Tyr  Arg  Ala  Gly  Glu  Asn  Leu  Asn
                         245                         250                         255
Leu  Thr  Cys  His  Ala  Ala  Ser  Asn  Pro  Thr  Ala  Gln  Tyr  Phe  Trp  Phe
                         260                         265                         270
Val  Asn  Gly  Thr  Phe  Gln  Gln  Ser  Thr  Gln  Glu  Leu  Phe  Ile  Pro  Asn
                         275                         280                         285
Ile  Thr  Val  Asn  Asn  Ser  Gly  Ser  Tyr  Met  Cys  Gln  Ala  His  Asn  Ser
                         290                         295                         300
Ala  Thr  Gly  Leu  Asn  Arg  Thr  Thr  Val  Thr  Ala  Ile  Thr  Val  Tyr  Ala
      305                         310                         315                         320
Glu  Leu  Pro  Lys  Pro  Tyr  Ile  Thr  Ser  Asn  Asn  Ser  Asn  Pro  Ile  Glu
                         325                         330                         335
Asp  Lys  Asp  Ala  Val  Thr  Leu  Thr  Cys  Glu  Pro  Glu  Thr  Gln  Asp  Thr
                         340                         345                         350
Thr  Tyr  Leu  Trp  Trp  Val  Asn  Asn  Gln  Ser  Leu  Ser  Val  Ser  Ser  Arg
                         355                         360                         365
Leu  Glu  Leu  Ser  Asn  Asp  Asn  Arg  Thr  Leu  Thr  Val  Phe  Asn  Ile  Pro
                         370                         375                         380
Arg  Asn  Asp  Thr  Thr  Phe  Tyr  Glu  Cys  Glu  Thr  Gln  Asn  Pro  Val  Ser
      385                         390                         395                         400
Val  Arg  Arg  Ser  Asp  Pro  Val  Thr  Leu  Asn  Val  Leu  Tyr  Gly  Pro  Asp
                         405                         410                         415
Ala  Pro  Thr  Ile  Ser  Pro  Leu  Asn  Thr  Pro  Tyr  Arg  Ala  Gly  Glu  Asn
                         420                         425                         430
Leu  Asn  Leu  Ser  Cys  His  Ala  Ala  Ser  Asn  Pro  Ala  Ala  Gln  Tyr  Ser
                         435                         440                         445
Trp  Phe  Val  Asn  Gly  Thr  Phe  Gln  Gln  Ser  Thr  Gln  Glu  Leu  Phe  Ile
                         450                         455                         460
Pro  Asn  Ile  Thr  Val  Asn  Asn  Ser  Gly  Ser  Tyr  Met  Cys  Gln  Ala  His
      465                         470                         475                         480
Asn  Ser  Ala  Thr  Gly  Leu  Asn  Arg  Thr  Thr  Val  Thr  Ala  Ile  Thr  Val
                         485                         490                         495
Tyr  Val  Glu  Leu  Pro  Lys  Pro  Tyr  Ile  Ser  Ser  Asn  Asn  Ser  Asn  Pro
                         500                         505                         510
Ile  Glu  Asp  Lys  Asp  Ala  Val  Thr  Leu  Thr  Cys  Glu  Pro  Val  Ala  Glu
                         515                         520                         525
```

```
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
        530             535             540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
545             550             555             560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
            565             570             575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
            580             585             590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
        595             600             605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
    610             615             620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
625             630             635             640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
            645             650             655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
            660             665             670
Ser Val Ser Ser Gly Asp Ser Ala Pro Gly Ser Ser Gly Leu Ser Ala
        675             680             685
Arg Ala Thr Val Gly Ile Ile Ile Gly Met Leu Val Gly Val Ala Leu
    690             695             700
Met
705
```

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<210> 19
<211> 705
<212> PRT
<213> Macaca mulatta

<400> 19
Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
1               5               10              15
Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20              25              30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
```

```
            35                      40                      45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
        50                      55                      60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65                      70                      75                      80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
                    85                      90                      95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
                    100                     105                     110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
                    115                     120                     125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
        130                     135                     140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                     150                     155                     160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
                    165                     170                     175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
                    180                     185                     190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
                    195                     200                     205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
        210                     215                     220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                     230                     235                     240
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
                    245                     250                     255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
                    260                     265                     270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
                    275                     280                     285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
        290                     295                     300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
305                     310                     315                     320
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
                    325                     330                     335
```

```
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
        340                 345                 350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
        355                 360                 365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
    370                 375                 380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
385                 390                 395                 400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
                405                 410                 415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
            420                 425                 430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Phe
        435                 440                 445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
        450                 455                 460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
465                 470                 475                 480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
                485                 490                 495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
                500                 505                 510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
            515                 520                 525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
        530                 535                 540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
545                 550                 555                 560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
                565                 570                 575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
                580                 585                 590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
            595                 600                 605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
        610                 615                 620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
```

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```
             625                        630                        635                        640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Asn Gly Ala Tyr Ala Cys Phe
                      645                    650                    655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
                  660                    665                    670
Ser Val Ser Ser Gly Asp Ser Ala Pro Gly Ser Ser Gly Leu Ser Ala
              675                    680                    685
Arg Ala Thr Val Gly Ile Ile Ile Gly Met Leu Val Gly Val Ala Leu
          690                    695                    700
Met
705
```

<210> 20
<211> 702
<212> PRT
<213> Homo sapiens

<400> 20

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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
 1               5                    10                   15
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
                  20                  25                  30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
              35                  40                  45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
          50                  55                  60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65                  70                   75                  80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
                  85                  90                  95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
                  100                 105                 110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
              115                 120                 125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
          130                 135                 140
```

```
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145             150             155             160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
                165             170             175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180             185             190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
            195             200             205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
        210             215             220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225             230             235             240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
            245             250             255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
            260             265             270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
            275             280             285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
        290             295             300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305             310             315             320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325             330             335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
            340             345             350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
            355             360             365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
        370             375             380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385             390             395             400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
            405             410             415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
            420             425             430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
```

```
                435                     440                     445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
    450                     455                 460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                     470                 475                 480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
                485                     490                 495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
                500                     505                 510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
                515                     520                 525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
    530                 ⁻ 535                     540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545                     550                 555                 560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
                565                     570                 575
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
                580                     585                 590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
                595                     600                 605
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
    610                 615                     620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625                     630                 635                 640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                645                     650                 655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
                660                     665                 670
Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
                675                     680                 685
Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
    690                     695                 700
```

<210> 21

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAoptDOMopt fusion

<400> 21

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cacctgttcg gctacagctg gtacaagggc gagcgcgtgg acggcaaccg ccagatcatc 240
ggctacgtga tcggcaccca gcaggccacc cccggccccg cctacagcgg ccgcgagatc 300
atctacccca cgccagcct gctgatccag aacatcatcc agaacgacac cggcttctac 360
accctgcacg tgatcaagag cgacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccccgagc tgcccaagcc cagcatcagc agcaacaaca gcaagcccgt ggaggacaag 480
gacgccgtgg ccttcacctg cgagcccgag acccaggacg ccacctacct gtggtgggtg 540
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gagctgttca tcagcaacat caccgagaag aacagcggcc tgtacacctg ccaggccaac 1440
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cccaagccca gcatcagcag caacaacagc aagcccgtgg aggacaagga cgccgtggcc 1560
ttcacctgcg agcccgaggc ccagaacacc acctacctgt ggtgggtgaa cggccagagc 1620
ctgcccgtga gccccgcct gcagctgagc aacggcaacc gcaccctgac cctgttcaac 1680
gtgacccgca cgacgcccg cgcctacgtg tgcggcatcc agaacagcgt gagcgccaac 1740
cgcagcgacc ccgtgaccct ggacgtgctg tacggccccg acacccccat catcagcccc 1800
```

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cccgacagca gctacctgag cggcgccaac ctgaacctga gctgccacag cgccagcaac 1860
cccagccccc agtacagctg gcgcatcaac ggcatccccc agcagcacac ccaggtgctg 1920
ttcatcgcca agatcacccc caacaacaac ggcacctacg cctgcttcgt gagcaacctg 1980
gccaccggcc gcaacaacag catcgtgaag agcatcaccg tgagcgccag cggcacctct 2040
agaagcaccc ccatcccatt cagctacagc aagaacctgg actgctgggt ggacaacgag 2100
gaggacatcg acgtgatcct gaagaagagc accatcctga acctggacat caacaacgac 2160
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gtgcacaagg ccatggacat cgagtacaac gacatgttca acaacttcac cgtgagcttc 2340
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agcatcatca gcagcatgaa gaagcacagc ctgagcatcg gcagcggctg gagcgtgagc 2460
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accttcagag acctgcccga caagttcaat gcctacctgg ccaacaagtg ggtgttcatc 2580
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gacagatgca acaacaacaa ccagtacgtg agcatcgaca agttccggat cttctgcaag 2760
gccctgaacc ccaaggagat cgagaagctg tacaccagct acctgagcat caccttcctg 2820
agagacttct ggggcaaccc cctgagatac gacacctag                        2859
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<210> 22
<211> 2037
<212> DNA
<213> Artificial Sequence

<220>
<223> deleted human CEA

<400> 22

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tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaacccgt ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
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aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600

actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660

gtgagtgcca ggcgcagtga ttcagtcatc ctgaatgtcc tctatggccc ggatgccccc 720

accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctcctgccac 780

gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840

acccaagagc tctttatccc caacatcact gtgaataata gtggatccta cgtgccaa 900

gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960

gagccaccca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020

gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg ggtaaataat 1080

cagagcctcc cggtcagtcc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140

ctcagtgtca caaggaatga tgtaggaccc tatgagtgtg aatccagaa cgaattaagt 1200

gttgaccaca gcgacccagt catcctgaat gtcctctatg gcccagacga ccccaccatt 1260

tcccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg ccatgcagcc 1320

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cccaagccct ccatctccag caacaactcc aaacccgtgg aggacaagga tgctgtggcc 1560

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tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980

gctactggcc gcaataattc catagtcaag agcatcacag tctctgcatc tggaact     2037
```

<210> 23

<211> 679

<212> PRT

<213> Artificial Sequence

<220>

<223> deleted human CEA

<400> 23

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1               5                   10                  15
```

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        20              25              30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
        35              40              45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
    50              55              60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65              70              75              80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
            85              90              95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
        100             105             110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
        115             120             125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
    130             135             140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145             150             155             160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
            165             170             175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
            180             185             190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
        195             200             205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
    210             215             220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225             230             235             240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
            245             250             255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
            260             265             270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
        275             280             285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
    290             295             300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
```

```
      305                     310                     315                     320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                        325                     330                     335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
                    340                     345                     350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
                355                     360                     365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
            370                     375                     380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385                     390                     395                     400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                        405                     410                     415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
                    420                     425                     430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
                435                     440                     445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
            450                     455                     460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                     470                     475                     480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
                        485                     490                     495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
                    500                     505                     510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
                515                     520                     525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
            530                     535                     540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545                     550                     555                     560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
                565                     570                     575
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
            580                     585                     590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
            595                     600                     605
```

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```
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
    610                 615                 620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625                 630                 635                 640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                645                 650                 655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
                660                 665                 670
Thr Val Ser Ala Ser Gly Thr
                675
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<210> 24
<211> 3426
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA-FRC fusion

<400> 24

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acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catcttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata 300
atataccccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaacccgt ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaag aaatgacaca gcaagctaca atgtgaaac ccagaaccca 660
gtgagtgcca ggcgcagtga ttcagtcatc ctgaatgtcc tctatggccc ggatgccccc 720
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gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
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gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
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cagagcctcc cggtcagtcc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140
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ataggcaacg atccaaatag ggatatatta attgcaagca actggtactt taatcatta 3360
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gattaa                                                         3426


<210> 25
<211> 2664
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA-FcIgG fusion

<400> 25
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<210> 26
<211> 2167
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA-LAMP fusion

<400> 26

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-41-

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caccctacac gtcataaagt cagatcttgt gaatgaagaa gcaactggcc agttccgggt 420

atacccggag ctgcccaagc cctccatctc cagcaacaac tccaaacccg tggaggacaa 480

ggatgctgtg gccttcacct gtgaacctga gactcaggac gcaacctacc tgtggtgggt 540

aaacaatcag agcctcccgg tcagtcccag gctgcagctg tccaatggca acaggaccct 600

cactctattc aatgtcacaa gaaatgacac agcaagctac aaatgtgaaa cccagaaccc 660

agtgagtgcc aggcgcagtg attcagtcat cctgaatgtc ctctatggcc cggatgcccc 720

caccatttcc cctctaaaca catcttacag atcaggggaa aatctgaacc tctcctgcca 780

cgcagcctct aacccacctg cacagtactc ttggtttgtc aatgggactt tccagcaatc 840

cacccaagag ctctttatcc ccaacatcac tgtgaataat agtggatcct atacgtgcca 900

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gcccaagccc tccatctcca gcaacaactc caaacccgtg gaggacaagg atgctgtggc 1560

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cctcccagtc agtcccaggc tgcagctgtc caatggcaac aggaccctca ctctattcaa 1680

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agatgatggt aacaacatgt tgatccccat tgctgtgggc ggtgccctgg cagggctgat 2100

cctcatcgtc ctcattgcct acctcattgg caggaagagg agtcacgccg gctatcagac 2160

catctag                                                              2167
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<210> 27

<211> 3921

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-HSP70 fusion

<400> 27

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ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggcctctaac 1860
```

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ccatccccgc agtattcttg gcgtatcaat gggataccgc agcaacacac acaagttctc 1920

tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980

gctactggcc gcaataattc catagtcaag agcatcacag tctctgcatc tggaactcta 2040

gatatggctc gtgcggtcgg gatcgacctc gggaccacca actccgtcgt ctcggttctg 2100

gaaggtggcg acccggtcgt cgtcgccaac tccgagggct ccaggaccac cccgtcaatt 2160

gtcgcgttcg cccgcaacgg tgaggtgctg gtcggccagc ccgccaagaa ccaggcggtg 2220

accaacgtcg atcgcaccgt gcgctcggtc aagcgacaca tgggcagcga ctggtccata 2280

gagattgacg gcaagaaata caccgcgccg gagatcagcg cccgcattct gatgaagctg 2340

aagcgcgacg ccgaggccta cctcggtgag gacattaccg acgcggttat cacgacgccc 2400

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gatcgcaagc gtcgcgagga ggccgatgtt cgtaatcaag ccgagacatt ggtctaccag 3600

acggagaagt tcgtcaaaga acagcgtgag gccgagggtg gttcgaaggt acctgaagac 3660

acgctgaaca aggttgatgc cgcggtggcg gaagcgaagg cggcacttgg cggatcggat 3720

atttcggcca tcaagtcggc gatggagaag ctgggccagg agtcgcaggc tctggggcaa 3780

gcgatctacg aagcagctca ggctgcgtca ctggccactg cgctgcccca ccccggcggc 3840

gagccgggcg gtgcccaccc cggctcggct gatgacgttg tggacgcgga ggtggtcgac 3900

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<210> 28

- 44 -

<211> 3585

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-VSVG fusion

<400> 28

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acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag  180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata  240
ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata  300
atataccccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac  360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta  420
tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaacccgt ggaggacaag  480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta  540
aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc  600
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gtgagtgcca ggcgcagtga ttcagtcatc ctgaatgtcc tctatggccc ggatgccccc  720
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gcagcctcta cccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc  840
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cagagcctcc cggtcagtcc caggctgcag ctgtccaatg caacaggac cctcactcta  1140
ctcagtgtca caaggaatga tgtaggaccc tatgagtgtg aatccagaa cgaattaagt  1200
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tccccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg ccatgcagcc  1320
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gagctcttta tctccaacat cactgagaag aacagcggac tctatacctg ccaggccaat  1440
aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgcggagctg  1500
cccaagcccct ccatctccag caacaactcc aaaccgtgg aggacaagga tgctgtggcc  1560
ttcacctgtg aacctgaggc tcagaacaca acctacctgt ggtgggtaaa tggtcagagc  1620
ctcccagtca gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat  1680
gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gagtgcaaac  1740
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cgcagtgacc cagtcaccct ggatgtcctc tatgggccgg acacccccat catttccccc 1800

ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggcctctaac 1860

ccatccccgc agtattcttg gcgtatcaat gggataccgc agcaacacac acaagttctc 1920

tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980

gctactggcc gcaataattc catagtcaag agcatcacag tctctgcatc tggaactcta 2040

gatgaattca tgaagtgctt tttgtactta gctttttat tcatcggggt gaattgcaag 2100

ttcaccatag tttttccaca caaccaaaaa ggaaactgga aaaatgttcc ttccaattac 2160

cattattgcc cgtcaagctc agatttaaat tggcataatg acttaatagg cacaggctta 2220

caagtcaaaa tgcccaagag tcacaaggct attcaagcag acggttggat gtgtcatgct 2280

tccaaatggg tcactacttg tgatttccgc tggtacggac cgaagtatat aacacattcc 2340

atccgatcct tcactccatc tgtagaacaa tgcaaggaaa gcattgaaca aacgaaacaa 2400

ggaacttggc tgaatccagg cttccctcct caaagttgtg gatatgcaac tgtgacggat 2460

gccgaagcag tgattgtcca ggtgactcct caccatgtgc ttgttgatga atacacagga 2520

gaatgggttg attcacagtt catcaacgga aaatgcagca atgacatatg ccccactgtc 2580

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attttatttt ttggtgatac tgggctatcc aaaaatccaa tcgactttgt cgaaggttgg 3420

ttcagtagtt ggaagagctc cattgcctct ttttctttta tcataggggtt aatcattgga 3480

ctattcttgg ttctccgagt tggtatttat ctttacatta aattaaagca caccaagaaa 3540

agacagattt atacagacat agagatgaac cgacttggaa ggtaa          3585
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<210> 29

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 29

tattctagat tcaacaccaa ttccattttc ttattc   36

<210> 30

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 30

gcggccgcta gaatcatttg tccatccttc atc   33

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 31

tattctagat tcaacaccaa ttccattttc ttattc   36

<210> 32

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 32

ttagcggccg ctagttctgt atcatatcgt aaaggg   36

<210> 33
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 33
tctagataaa actcacacat gccca   25

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 34
gccgactcat ttacccggag acagggag   28

<210> 35
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 35
tctagatttg atccccattg ctgtgggcgg tgccctg   37

<210> 36
<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 36

ggcgtgactc ctcttcctgc caatgaggta ggcaatgag   39

<210> 37

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 37

atatctagat ttcaccatag tttttccaca caacc   35

<210> 38

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 38

gcggccgcct tccttccaag tcggttcatc tctatg   36

<210> 39

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 39
gctctagata tggctcgtgc ggtcgggatc gacc   34

<210> 40
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 40
gccgcggccg ctcacttggc ctcccggccg tcgtcg   36

<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 41
gttatctaga agcacccccca tccc   24

<210> 42
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 42
ttaagatctc taagatctgg tgtcgtatct cagggg   36

<210> 43

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 43

ttatctagaa agacccacac ctgcccccct tgc   33

<210> 44

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 44

tatagatctt agggtacctt acttgccggg g   31

<210> 45

<211> 952

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-Dom fusion

<400> 45

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1   5   10   15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
                20   25   30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly

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                35                      40                      45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
        50                      55                      60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65                      70                      75                      80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
                85                      90                      95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
                100                     105                     110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
                115                     120                     125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
        130                     135                     140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145                     150                     155                     160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
                165                     170                     175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
                180                     185                     190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
                195                     200                     205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
        210                     215                     220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                     230                     235                     240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
                245                     250                     255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
                260                     265                     270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
                275                     280                     285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
        290                     295                     300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305                     310                     315                     320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325                     330                     335
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Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
        340                 345                 350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
        355                 360                 365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
    370                 375                 380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385                 390                 395                 400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
            405                 410                 415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
        420                 425                 430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
        435                 440                 445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
    450                 455                 460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                 470                 475                 480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
            485                 490                 495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
        500                 505                 510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
        515                 520                 525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
    530                 535                 540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545                 550                 555                 560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
            565                 570                 575
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
        580                 585                 590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
        595                 600                 605
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
    610                 615                 620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
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625                      630                      635                      640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                645                      650                      655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
                660                      665                      670
Thr Val Ser Ala Ser Gly Thr Ser Arg Ser Thr Pro Ile Pro Phe Ser
                675                      680                      685
Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp
        690                      695                      700
Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp
705                      710                      715                      720
Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro
                725                      730                      735
Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val
                740                      745                      750
Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu
                755                      760                      765
Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
        770                      775                      780
Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr
785                      790                      795                      800
Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly
                805                      810                      815
Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp
        820                      825                      830
Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys
        835                      840                      845
Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn
        850                      855                      860
Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly
865                      870                      875                      880
Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile
                885                      890                      895
Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile
                900                      905                      910
Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu
                915                      920                      925
```

```
Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp
    930             935             940
Gly Asn Pro Leu Arg Tyr Asp Thr
945             950


<210> 46
<211> 907
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA-FcIgG fusion

<400> 46
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1               5               10              15
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
                20              25              30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
            35              40              45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
    50              55              60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65              70              75              80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
                85              90              95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
                100             105             110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
            115             120             125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
    130             135             140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145             150             155             160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
                165             170             175
```

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Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
        180                 185                 190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
        195                 200                 205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
    210                 215                 220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                 230                 235                 240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
                245                 250                 255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
            260                 265                 270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
            275                 280                 285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
    290                 295                 300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305                 310                 315                 320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325                 330                 335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
            340                 345                 350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
            355                 360                 365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
    370                 375                 380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385                 390                 395                 400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                405                 410                 415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
            420                 425                 430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
            435                 440                 445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
    450                 455                 460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
```

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ITR0073YP

```
     465                      470                      475                      480
     Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
                     485                      490                      495
     Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
                     500                      505                      510
     Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
                     515                      520                      525
     Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
             530                      535                      540
     Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
     545                      550                      555                      560
     Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
                     565                      570                      575
     Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
                     580                      585                      590
     Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
                     595                      600                      605
     Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
             610                      615                      620
     Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
     625                      630                      635                      640
     Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                     645                      650                      655
     Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
                     660                      665                      670
     Thr Val Ser Ala Ser Gly Thr Ser Arg Lys Thr His Thr Cys Pro Pro
                     675                      680                      685
     Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
             690                      695                      700
     Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
     705                      710                      715                      720
     Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
                     725                      730                      735
     Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                     740                      745                      750
     Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
             755                      760                      765
```

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```
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
    770             775             780
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
785             790             795             800
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
            805             810             815
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            820             825             830
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            835             840             845
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    850             855             860
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
865             870             875             880
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            885             890             895
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            900             905
```

<210> 47

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<223> DOM

<400> 47

```
gattcaacac caattccatt ttcttattct aaaaatctgg attgttgggt tgataatgaa 60
gaagatatag atgttatatt aaaaaagagt acaattttaa atttagatat taataatgat 120
attatatcag atatatctgg gtttaattca tctgtaataa catatccaga tgctcaattg 180
gtgcccggaa taaatggcaa agcaatacat ttagtaaaca atgaatcttc tgaagttata 240
gtgcataaag ctatggatat tgaatataat gatatgttta ataattttac cgttagcttt 300
tggttgaggg ttcctaaagt atctgctagt catttagaac aatatggcac aaatgagtat 360
tcaataatta gctctatgaa aaaacatagt ctatcaatag gatctggttg gagtgtatca 420
cttaaaggta ataacttaat atggactttta aaagattccg cgggagaagt tagacaaata 480
```

```
acttttaggg atttacctga taaatttaat gcttatttag caaataaatg ggttttata    540
actattacta atgatagatt atcttctgct aatttgtata taaatggagt acttatggga    600
agtgcagaaa ttactggttt aggagctatt agagaggata ataatataac attaaaacta    660
gatagatgta ataataataa tcaatacgtt tctattgata aatttaggat attttgcaaa    720
gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aacctttta      780
agagacttct ggggaaaccc tttacgatat gatacagata ggtag                     825
```

<210> 48
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> DOM

<400> 48

```
Asp Ser Thr Pro Ile Pro Phe Ser Tyr Ser Lys Asn Leu Asp Cys Trp
1               5                   10                  15
Val Asp Asn Glu Glu Asp Ile Asp Val Ile Leu Lys Lys Ser Thr Ile
                20                  25                  30
Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser Gly Phe
            35                  40                  45
Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro Gly Ile
        50                  55                  60
Asn Gly Lys Ala Ile His Leu Val Asn Asn Glu Ser Ser Glu Val Ile
65                  70                  75                  80
Val His Lys Ala Met Asp Ile Glu Tyr Asn Asp Met Phe Asn Asn Phe
                85                  90                  95
Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu
                100                 105                 110
Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met Lys Lys
            115                 120                 125
His Ser Leu Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys Gly Asn
        130                 135                 140
Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg Gln Ile
145                 150                 155                 160
Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys
```

```
                    165                  170                  175
Trp Val Phe Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu
                180                  185                  190
Tyr Ile Asn Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly Leu Gly
            195                  200                  205
Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn
        210                  215                  220
Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys
225                  230                  235                  240
Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser
                245                  250                  255
Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
                260                  265                  270
Asp Arg
```

<210> 49
<211> 2857
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA-DOM fusion

<400> 49

```
atggagtctc cctcggcccc tccccacaga tggtgcatcc cctggcagag gctcctgctc 60
acagcctcac ttctaacctt ctggaacccg cccaccactg ccaagctcac tattgaatcc 120
acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catcttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca caagctacc ccagggcccg catacagtgg tcgagagata 300
atataccccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaacccgt ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaag aaatgacaca gcaagctaca atgtgaaac ccagaaccca 660
```

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ITR0073YP

gtgagtgcca ggcgcagtga ttcagtcatc ctgaatgtcc tctatggccc ggatgccccc 720

accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctcctgccac 780

gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840

acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgccaa 900

gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960

gagccaccca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020

gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg ggtaaataat 1080

cagagcctcc cggtcagtcc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140

ctcagtgtca caaggaatga tgtaggaccc tatgagtgtg aatccagaa cgaattaagt 1200

gttgaccaca gcgacccagt catcctgaat gtcctctatg cccagacga ccccaccatt 1260

tccccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg ccatgcagcc 1320

tctaacccac ctgcacagta ttcttggctg attgatggga acatccagca acacacacaa 1380

gagctcttta tctccaacat cactgagaag aacagcggac tctatacctg ccaggccaat 1440

aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgcggagctg 1500

cccaagccct ccatctccag caacaactcc aaacccgtgg aggacaagga tgctgtggcc 1560

ttcacctgtg aacctgaggc tcagaacaca acctacctgt ggtgggtaaa tggtcagagc 1620

ctcccagtca gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680

gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gagtgcaaac 1740

cgcagtgacc cagtcaccct ggatgtcctc tatgggccgg acacccccat catttccccc 1800

ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggcctctaac 1860

ccatccccgc agtattcttg cgtatcaat gggataccgc agcaacacac acaagttctc 1920

tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980

gctactggcc gcaataattc catagtcaag agcatcacag tctctgcatc tggaactcta 2040

gattcaacac caattccatt ttcttattct aaaaatctgg attgttgggt tgataatgaa 2100

gaagatatag atgttatatt aaaaaagagt acaattttaa atttagatat taataatgat 2160

attatatcag atatatctgg gtttaattca tctgtaataa catatccaga tgctcaattg 2220

gtgcccggaa taaatggcaa agcaatacat ttagtaaaca atgaatcttc tgaagttata 2280

gtgcataaag ctatggatat tgaatataat gatatgttta ataattttac cgttagcttt 2340

tggttgaggg ttcctaaagt atctgctagt catttagaac aatatggcac aaatgagtat 2400

tcaataatta gctctatgaa aaaacatagt ctatcaatag gatctggttg gagtgtatca 2460

cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 2520

acttttaggg atttacctga taaatttaat gcttatttag caaataaatg ggtttttata 2580

actattacta atgatagatt atcttctgct aatttgtata taaatggagt acttatggga 2640

agtgcagaaa ttactggttt aggagctatt agagaggata taatataac attaaaacta 2700

gatagatgta ataataataa tcaatacgtt tctattgata aatttaggat attttgcaaa 2760

gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aaccttttta 2820

agagacttct ggggaaaccc tttacgatat gatatag   2857

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<210> 50

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 50

```
atgggcagcc ccagcgcccc cctgcaccgc tggtgcatcc cctggcagac cctgctgctg 60
accgccagcc tgctgacctt ctggaacccc cccaccaccg cccagctgac catcgagagc 120
cgcccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
agctgcgtga tccgcaccca gcagatcacc cccggccccg cccacagcgg ccgcgagacc 300
atcgacttca cgccagcct gctgatccac aacgtgaccc agagcgacac cggcagctac 360
accatccagg tgatcaagga ggacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccccgagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccgt ggaggacaag 480
gacgccgtgg ccctgacctg cgagcccgag acccaggaca ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccgt gagcccccgc ctggagctga gcagcgacaa ccgcaccctg 600
accgtgttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
gtgagcgtgc ccgcagcga ccccgtgacc ctgaacgtgc tgtacggccc cgacgccccc 720
accatcagcc ccctgaacac cccctaccgc gccggcgaga acctgaacct gacctgccac 780
gccgccagca cccccaccgc ccagtacttc tggttcgtga cggcaccttc cagcagagc 840
acccaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta catgtgccag 900
gcccacaaca gcgccaccgg cctgaaccgc accaccgtga ccgccatcac cgtgtacgcc 960
gagctgccca gccctacat caccagcaac aacagcaacc catcgagga caaggacgcc 1020
gtgaccctga cctgcgagcc cgagacccag gacaccacct acctgtggtg ggtgaacaac 1080
cagagcctga gcgtgagcag ccgcctggag ctgagcaacg acaaccgcac cctgaccgtg 1140
ttcaacatcc cccgcaacga caccaccttc tacgagtgcg agacccagaa ccccgtgagc 1200
gtgcgccgca gcgacccgt gaccctgaac gtgctgtacg ccccgacgc ccccaccatc 1260
agccccctga acaccccta ccgcgccggc gagaacctga acctgagctg ccacgccgcc 1320
agcaaccccg ccgcccagta cagctggttc gtgaacggca ccttccagca gagcacccag 1380
gagctgttca tccccaacat caccgtgaac aacagcggca gctacatgtg ccaggcccac 1440
aacagcgcca ccggcctgaa ccgcaccacc gtgaccgcca tcaccgtgta cgtggagctg 1500
cccaagcccct acatcagcag caacaacagc aaccccatcg aggacaagga cgccgtgacc 1560
ctgacctgcg agcccgtggc cgagaacacc acctacctgt ggtgggtgaa caaccagagc 1620
```

```
ctgagcgtga gcccccgcct gcagctgagc aacggcaacc gcatcctgac cctgctgagc 1680

gtgacccgca acgacaccgg cccctacgag tgcggcatcc agaacagcga gagcgccaag 1740

cgcagcgacc ccgtgaccct gaacgtgacc tacggccccg acaccccat catcagcccc 1800

cccgacctga gctaccgcag cggcgccaac ctgaacctga gctgccacag cgacagcaac 1860

cccagccccc agtacagctg gctgatcaac ggcaccctgc gccagcacac ccaggtgctg 1920

ttcatcagca agatcaccag caacaacagc ggcgcctacg cctgcttcgt gagcaacctg 1980

gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040

agaagcaccc ccatcccatt cagctacagc aagaacctgg actgctgggt ggacaacgag 2100

gaggacatcg acgtgatcct gaagaagagc accatcctga acctggacat caacaacgac 2160

atcatcagcg acatcagcgg cttcaacagc agcgtgatca cctaccccga cgcccagctg 2220

gtgcccggca tcaacggcaa ggccatccac ctggtgaaca cgagagcag cgaggtgatc 2280

gtgcacaagg ccatggacat cgagtacaac gacatgttca caacttcac cgtgagcttc 2340

tggctgagag tgcctaaggt gagcgccagc cacctggagc agtacggcac caacgagtac 2400

agcatcatca gcagcatgaa gaagcacagc ctgagcatcg gcagcggctg gagcgtgagc 2460

ctgaagggca caacctcat ctggaccctg aaggatagcg ccggagaggt gagacagatc 2520

accttcagag acctgcccga caagttcaat gcctacctgg ccaacaagtg ggtgttcatc 2580

accatcacca cgacagact gagcagcgcc aacctgtaca tcaacggcgt gctcatgggc 2640

agcgccgaga tcaccggcct gggcgccatc agagaggaca caacatcac cctgaagctg 2700

gacagatgca acaacaacaa ccagtacgtg agcatcgaca agttccggat cttctgcaag 2760

gccctgaacc ccaaggagat cgagaagctg tacaccagct acctgagcat caccttcctg 2820

agagacttct ggggcaaccc cctgagatac gacacctag            2859
```

<210> 51

<211> 952

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 51

```
Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
1               5                   10                  15

Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20                  25                  30

Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
            35                  40                  45
```

```
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
    50              55                  60

Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65                  70                  75                  80

Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
                85                  90                  95

Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
                100                 105                 110

Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
            115                 120                 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
    130                 135                 140

Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                 150                 155                 160

Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
                165                 170                 175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
                180                 185                 190

Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
            195                 200                 205

Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
    210                 215                 220

Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                 230                 235                 240

Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
                245                 250                 255

Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
                260                 265                 270

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
            275                 280                 285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
    290                 295                 300

Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
305                 310                 315                 320

Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
                325                 330                 335

Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
```

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```
            340                    345                    350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
        355                    360                    365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
    370                    375                    380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
385                    390                    395                    400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
                405                    410                    415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
                420                    425                    430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
            435                    440                    445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
    450                    455                    460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
465                    470                    475                    480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
                485                    490                    495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
                500                    505                    510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
            515                    520                    525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
    530                    535                    540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
545                    550                    555                    560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
                565                    570                    575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
                580                    585                    590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
            595                    600                    605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
    610                    615                    620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
625                    630                    635                    640
```

Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
                 645   650   655

Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
                 660   665   670

Ser Val Ser Ser Gly Asp Ser Ser Arg Ser Thr Pro Ile Pro Phe Ser
                 675   680   685

Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp
    690   695   700

Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp
705   710   715   720

Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser·Val Ile Thr Tyr Pro
                 725   730   735

Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val
                 740   745   750

Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu
                 755   760   765

Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
    770   775   780

Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr
785   790   795   800

Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly
                 805   810   815

Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp
                 820   825   830

Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys
                 835   840   845

Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn
    850   855   860

Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly
865   870   875   880

Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile
                 885   890   895

Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile
                 900   905   910

Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu
                 915   920   925

Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp

```
           930                  935                   940
   Gly Asn Pro Leu Arg Tyr Asp Thr
   945                  950



   <210> 52
   <211> 2359
   <212> DNA
   <213> Artificial Sequence

   <220>
   <223> rhCEA-CTBopt fusion

   <400> 52
   atgggcagcc ccagcgcccc cctgcaccgc tggtgcatcc cctggcagac cctgctgctg 60
   accgccagcc tgctgacctt ctggaacccc cccaccaccg cccagctgac catcgagagc 120
   cgccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
   aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
   agctgcgtga tccgcaccca gcagatcacc cccggccccg cccacagcgg ccgcgagacc 300
   atcgacttca cgccagcct gctgatccac aacgtgaccc agagcgacac cggcagctac 360
   accatccagg tgatcaagga ggacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
   taccccgagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccgt ggaggacaag 480
   gacgccgtgg ccctgacctg cgagcccgag acccaggaca ccacctacct gtggtgggtg 540
   aacaaccaga gcctgcccgt gagcccccgc ctggagctga gcagcgacaa ccgcaccctg 600
   accgtgttca acatcccccg caacgacacc accagctaca gtgcgagac ccagaacccc 660
   gtgagcgtgc ccgcagcga ccccgtgacc ctgaacgtgc tgtacggccc cgacgccccc 720
   accatcagcc ccctgaacac cccctaccgc gccggcgaga acctgaacct gacctgccac 780
   gccgccagca accccaccgc ccagtacttc tggttcgtga cggcacctt ccagcagagc 840
   acccaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta catgtgccag 900
   gcccacaaca gcgccaccgg cctgaaccgc accaccgtga ccgccatcac cgtgtacgcc 960
   gagctgccca gccctacat caccagcaac aacagcaacc ccatcgagga caaggacgcc 1020
   gtgaccctga cctgcgagcc cgagacccag gacaccacct acctgtggtg ggtgaacaac 1080
   cagagcctga gcgtgagcag ccgcctggag ctgagcaacg acaaccgcac cctgaccgtg 1140
   ttcaacatcc cccgcaacga caccaccttc tacgagtgcg agacccagaa ccccgtgagc 1200
   gtgcgccgca gcgaccccgt gaccctgaac gtgctgtacg ccccgacgc ccccaccatc 1260
   agcccccctga cacccccta ccgcgccggc gagaacctga acctgagctg ccacgccgcc 1320
   agcaaccccg ccgcccagta cagctggttc gtgaacggca ccttccagca gagcacccag 1380
```

```
gagctgttca tccccaacat caccgtgaac aacagcggca gctacatgtg ccaggcccac 1440

aacagcgcca ccggcctgaa ccgcaccacc gtgaccgcca tcaccgtgta cgtggagctg 1500

cccaagccct acatcagcag caacaacagc aaccccatcg aggacaagga cgccgtgacc 1560

ctgacctgcg agcccgtggc cgagaacacc acctacctgt ggtgggtgaa caaccagagc 1620

ctgagcgtga gcccccgcct gcagctgagc aacggcaacc gcatcctgac cctgctgagc 1680

gtgacccgca cgacaccgg ccctacgag tgcggcatcc agaacagcga gcgccaag 1740

cgcagcgacc ccgtgaccct gaacgtgacc tacggccccg acccccat catcagcccc 1800

cccgacctga gctaccgcag cggcgccaac ctgaacctga gctgccacag cgacagcaac 1860

cccagccccc agtacagctg gctgatcaac ggcaccctgc ccagcacac ccaggtgctg 1920

ttcatcagca agatcaccag caacaacagc ggcgcctacg cctgcttcgt gagcaacctg 1980

gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040

agaacccctc agaacatcac cgatctgtgc gccgagtacc acaacaccca gatctacacc 2100

ctgaacgaca agatcttcag ctacaccgag agcctggccg gcaagagaga gatggccatc 2160

atcaccttca gaacggcgc catcttccag gtggaggtgc ccggcagcca gcacatcgac 2220

agccagaaga aggccatcga gcggatgaag gacaccctgc ggatcgccta cctcaccgag 2280

gccaaggtgg agaagctgtg cgtgtggaac aacaagaccc ctcacgccat cgccgccatc 2340

agcatggcca attgataag                                                2359
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<210> 53

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-CTBopt fusion

<400> 53

```
Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
1               5                   10                  15
Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
                20                  25                  30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
            35                  40                  45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
        50                  55                  60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65                  70                  75                  80
```

```
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
                85                  90                  95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
               100                 105                 110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
               115                 120                 125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
     130                 135                 140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                 150                 155                 160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
               165                 170                 175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
               180                 185                 190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
               195                 200                 205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
     210                 215                 220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                 230                 235                 240
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
               245                 250                 255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
               260                 265                 270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
               275                 280                 285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
     290                 295                 300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
305                 310                 315                 320
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
               325                 330                 335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
               340                 345                 350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
               355                 360                 365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
```

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```
            370                    375                    380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
385                    390                    395                    400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
                405                    410                    415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
                    420                    425                    430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
                435                    440                    445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
        450                    455                    460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
465                    470                    475                    480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
                    485                    490                    495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
                500                    505                    510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
                515                    520                    525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
                530                    535                    540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
545                    550                    555                    560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
                565                    570                    575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
                580                    585                    590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
                595                    600                    605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
                610                    615                    620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
625                    630                    635                    640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
                    645                    650                    655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
                660                    665                    670
```

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```
Ser Val Ser Ser Gly Asp Ser Ser Arg Thr Pro Gln Asn Ile Thr Asp
        675             680             685

Leu Cys Ala Glu Tyr His Asn Thr Gln Ile Tyr Thr Leu Asn Asp Lys
        690             695             700

Ile Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile
705             710             715             720

Ile Thr Phe Lys Asn Gly Ala Ile Phe Gln Val Glu Val Pro Gly Ser
                725             730             735

Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
                740             745             750

Leu Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val
        755             760             765

Trp Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
        770             775             780
```

<210> 54
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> tetanus toxoid peptide

<400> 54
```
Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala
1               5               10              15

Ser His Leu Glu
            20
```